

Fig. 1A



Fig. 1B

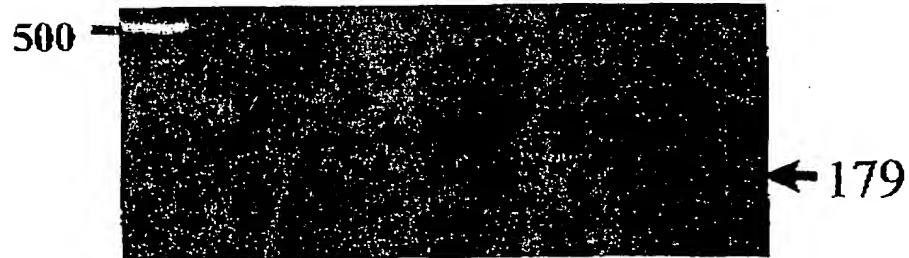


Fig. 1C

POSTER - 285 E 2650

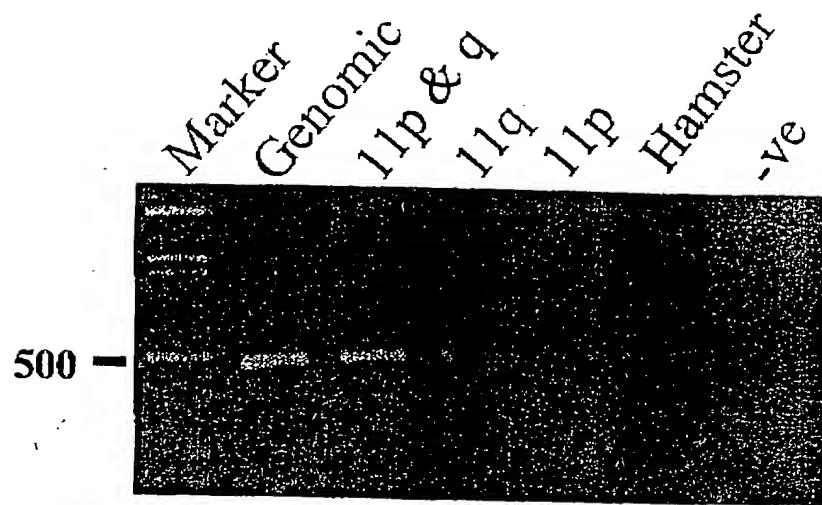


Fig. 2

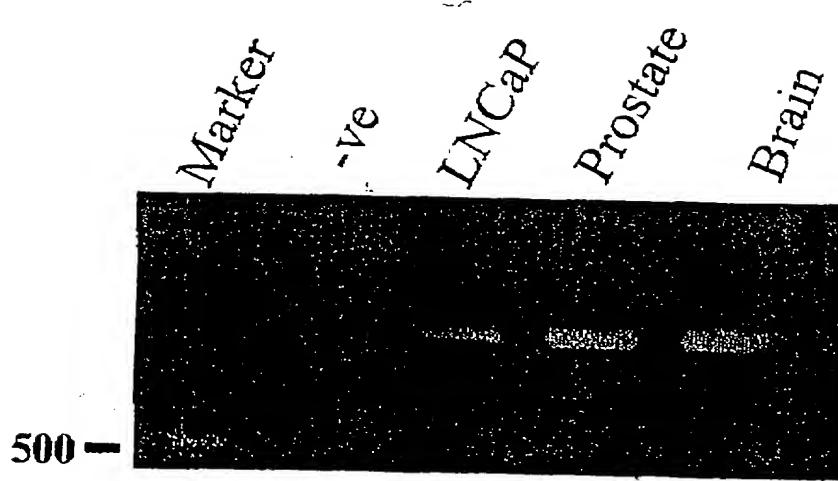


Fig. 3

09825282110000

PSMA	1	MWNLLHETDSAVERPRWLCA GALVLAGGFFLLGFLFG	40
PSMA-LIKE	1		0
	41	WFIKSSNEATNITPKHNMKAFLDELKAENIKKFLYNFTQI	80
	1		0
	81	PHLAGTEQNQLAKQIQSQWKEFGLDSVELAHYDVLLSYP	120
	1		0
	121	NKTHPNYISIINEDGNEIFNTSLFEPPPPGYENVSDIVPP	160
	1		0
	161	FSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINC SGKI	200
	1		0
	201	VIARYGKVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVK	240
	1		0
	241	SYPDGNLPGGGVQRGNILNLNGAGDPLTPGYPANEYAYR	280
	1		0
	281	RGIAEAVGLPSIPVHPIGYYDAQKLLEKMGG SAPPDSSWR	320
	1	MGGSAPPDSSWR	12

	321	GSLKVPYNVGP GFTGNFSTQKV KMHIHSTNEVTRIYNVIG	360
	13	GSLKVS YNVGP GFTGNFSTQKV KMHIHSTNEVTRIYNVIG	52

	361	TLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHEIVR	400
	53	TLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVR	92

Fig. 4-1

0907382-400904

401 SFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAENS 440
93 SFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEDNSR 132

441 LLQERGVAYINADSSIEGNYTLRVDCPLMYSLVHNLTKE 480
133 LLQERGVAYINADSSIEGNYTLRVDCPLMYSLVYNLTKE 172

481 LKSPDEGFEGKSLYESWTKKSPSPEFGMPRIKGSGND 520
173 LKSPDEGFEGKSLYESWTKKSPSPEFGMPRIKGSGND 212

521 FEVFFQRLGIASGRARYTKNWETNKFGYPLYHSVYETYE 560
213 FEVFFQRLGIASGRARYTKNWETNKFGYPLYHSVYETYE 252

561 LVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY 600
253 LVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY 292

601 AVVLRKYADKIYSISMKHPQEMKTYSVSFDSLFSAVKNFT 640
293 AVVLRKYADKIYNISMKHPQEMKTYSLSFDSLFSAVKNFT 332

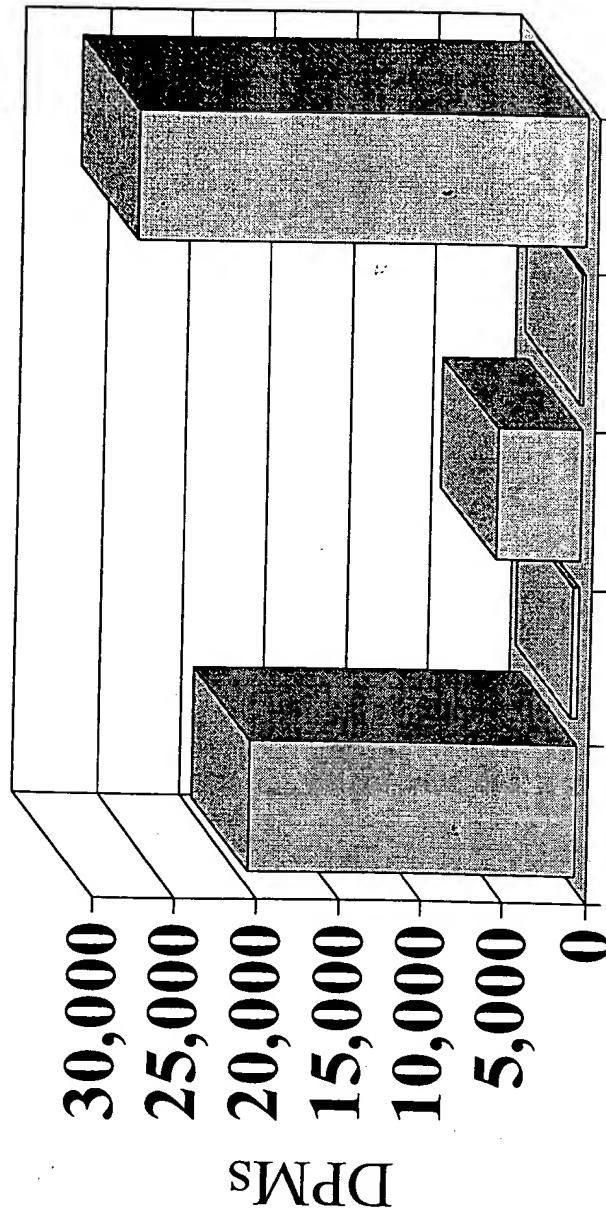
641 EIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAVIDPLG 680
333 EIASKFSERLQDFDKSNPILLRMMNDQLMFLERAVIDPLG 372

681 LPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVD 720
373 LPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVD 412

721 PSKAWEVKRQIYVAFTVQAAAETLSEVA (SEQ ID NO: 4)
413 PSKAWDVKRQISVAFTVQAAAETLSEVA (SEQ ID NO: 2)

Fig. 4-2

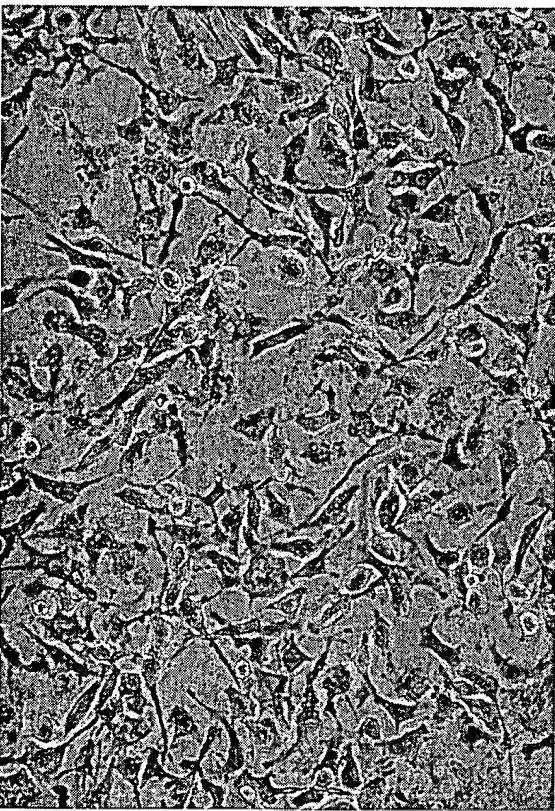
FIGURE 28E 2650



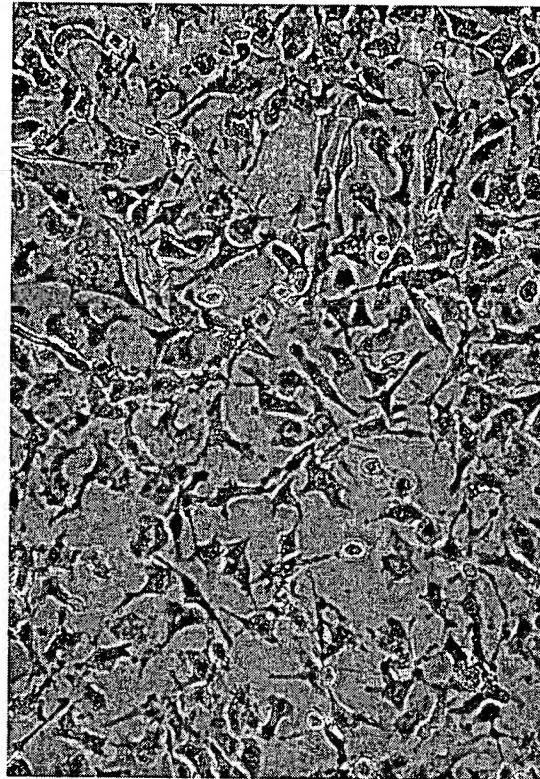
total counts in rxn
Lysis alone
PC3-PSML
C4-2

FIG. 5

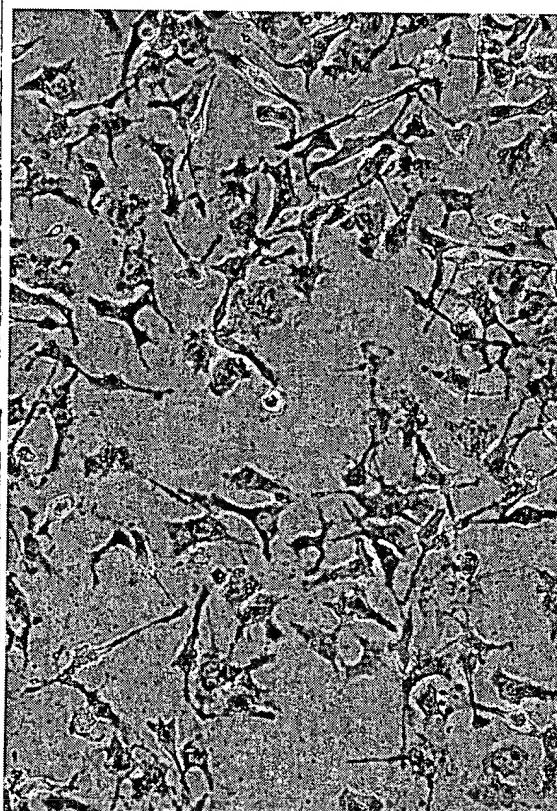
PRO 600 T 285E 2660



PC3-neo



PC3-PSMA



PC3-PSMA/Like Hybrid

PC3-PSM Like

Fig. 6